

SEQUENCE LISTING

<110> Raucy, Judy
 <120> Composition and Methods for Induction of Proteins Involved in
 Xenobiotic Metabolism
 <130> PUR-00114.P.1.1.1.1
 <150> US 10/222,679
 <151> 2002-08-16
 <150> US 09/832,621
 <151> 2001-04-11
 <150> US 60/196,681
 <151> 2000-04-12
 <150> US 60/241,391
 <151> 2000-10-17
 <160> 37
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 tgccgtgtat gtggggacaa ggccactggt tatcacttca atgtcatgac atgtgaaggg 180
 tgcaagggct ttttcaggag ggccatgaaa cgcaacgccc gccttaggtg ccccttccgg 240
 aaggggcgct gcgagatcac ccggaagacc cggcgacagt gccaggcctg ccggctgcgc 300
 aagtgcctgg agagcggcat gaagaaggag atgatcatgt ccgacgcggc cgtagaggag 360
 aggcgggcct tgatcaagag gaagaaaaga gaacggatcg ggactcagcc acccggagtg 420
 caggggctga cggaggagca gcggatgatg atcaggggagc tgatggacgc tcagatgaaa 480
 acctttgaca ctaccttctc ccatttcaag aatttccggc tgccaggggt gcttagcagt 540
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Cys Glu Asp Thr Glu Phe Ala Pro Gly Lys Pro Thr Val Asn Ala Asp
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Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
35              40              45

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Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
50              55              60

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Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
65              70              75              80

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Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
85              90              95

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Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile
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Met Ser Asp Ala Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys
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Lys Arg Glu Arg Ile Gly Thr Gln Pro Pro Gly Val Gln Gly Leu Thr
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Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys
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Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly
 165 170 175

Val Leu Ser Ser Gly Cys Glu Met Pro Glu Ser Leu Gln Ala Pro Ser
 180 185 190

Arg Glu Glu Ala Ala Lys Trp Asn Gln Val Arg Lys Asp Leu Trp Ser
 195 200 205

Val Lys Val Ser Val Gln Leu Arg Gly Glu Asp Gly Ser Val Trp Asn
 210 215 220

Tyr Lys Pro Pro Ala Asp Asn Gly Gly Lys Glu Ile Phe Ser Leu Leu
 225 230 235 240

Pro His *Met ala* Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Asn
 245 250 255

Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln
 260 265 270

Ile Ser Leu Leu Lys Gly Ala Thr Phe Glu Leu Cys Gln Leu Arg Phe
 275 280 285

Asn Thr Val Phe Asn Val Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu
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Ser Tyr Cys Leu Glu Asp Pro Ala Gly Gly Phe Gln Gln Leu Leu Leu
 305 310 315 320

Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His
 325 330 335

Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp
 340 345 350

Arg Pro Gly Val Val Gln His His Val Val Asp Gln Leu Gln Glu Gln
 355 360 365

Tyr Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro
 370 375 380

Ala His Arg Phe Leu Phe Leu Lys Ile *Met ala* Met Leu Thr Glu Leu
 385 390 395 400

Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
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Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr
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 aagggtttct tcaggagaac agtcagcaaa agcattggtc ccacctgccc ctttgctgga 180
 agctgtgaag tcagcaagat tcagaggcgc cactgcccag cctgcaggtt gcagaagtgc 240

ttagatgctg gcatgaggaa agacatgata ctgtcggcag aagccctggc attgcggcga	300
gcaaagcagg cccagcggcg ggcacagcaa acacctatgc aactgagtaa tgagcaagaa	360
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ctgtatgcga agttgctggg cctgctggct gagctccgga gcattaatga ggcctacggg	1020
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 35 40 45

Ser Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val
 50 55 60

Ser Lys Ile Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys
 65 70 75 80

Leu Asp Ala Gly Met Arg Lys Asp Met Ile Leu Ser Ala Glu Ala Leu
 85 90 95

Ala Leu Arg Arg Ala Lys Gln Ala Gln Arg Arg Ala Gln Gln Thr Pro
 100 105 110

Met Gln Leu Ser Asn Glu Gln Glu Glu Leu Ile Gln Thr Leu Leu Gly
 115 120 125

Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln Phe
 130 135 140

Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr Leu
 145 150 155 160

Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Val Asn Thr Phe
 165 170 175

Met Val Gln Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe Arg
 180 185 190

Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala Val
 195 200 205

Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr Gln
 210 215 220

Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Ala Ala Arg
 225 230 235 240

Val Ser Pro Ala Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe
 245 250 255

His Phe His Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr
 260 265 270

Val Leu Leu Ala Ala *Met ala* Leu Phe Ser Pro Asp Arg Pro Gly Val
 275 280 285

Thr Gln Arg His Glu Ile Asp Gln Leu Gln Glu Glu *Met ala* Leu Thr
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Leu Gln Ser Tyr Ile Lys Gly Gln Gln Gln Arg Pro Arg Asp Arg Phe
 305 310 315 320

Leu Tyr Ala Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn
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